

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hillman, Jennifer L.
Goli, Surya K.
Corley, Neil C.
- (ii) TITLE OF THE INVENTION: NEW RAS-LIKE PROTEIN
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0283 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 199 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: UTRSNOT02
 - (B) CLONE: 683101

10091613.030402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Lys Ser Ala Glu Val Lys Leu Ala Ile Phe Gly Arg Ala Gly
 1 5 10 15
 Val Gly Lys Ser Ala Leu Val Val Arg Phe Leu Thr Lys Arg Phe Ile
 20 25 30
 Trp Glu Tyr Asp Pro Thr Leu Glu Ser Thr Tyr Arg His Gln Ala Thr
 35 40 45
 Ile Asp Asp Glu Val Val Ser Met Glu Ile Leu Asp Thr Ala Gly Gln
 50 55 60
 Glu Asp Thr Ile Gln Arg Glu Gly His Met Arg Trp Gly Glu Gly Phe
 65 70 75 80
 Val Leu Val Tyr Asp Ile Thr Asp Arg Gly Ser Phe Glu Glu Val Leu
 85 90 95
 Pro Leu Lys Asn Ile Leu Asp Glu Ile Lys Lys Pro Lys Asn Val Thr
 100 105 110
 Leu Ile Leu Val Gly Asn Lys Ala Asp Leu Asp His Ser Arg Gln Val
 115 120 125
 Ser Thr Glu Glu Gly Glu Lys Leu Ala Thr Glu Leu Ala Cys Ala Phe
 130 135 140
 Tyr Glu Cys Ser Ala Cys Thr Gly Glu Gly Asn Ile Thr Glu Ile Phe
 145 150 155 160
 Tyr Glu Leu Cys Arg Glu Val Arg Arg Arg Met Val Gln Gly Lys
 165 170 175
 Thr Arg Arg Arg Ser Ser Thr Thr His Val Lys Gln Thr Ile Asn Glu
 180 185 190
 Met Leu Thr Lys Ile Ser Ser
 195

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 825 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSN02
- (B) CLONE: 683101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GACTCTTCCA AGATTACAA TGATATGGTG AATCCAAAGA CTGGAACCAA AAAGATTTAC 60
 TCAGTGCTTT AGTTTAAACA ACAGTAAATT GTCTACCAAC ACCCATCATG GCTAAAAGTG 120
 CGGAGGTCAA ACTGGCAATA TTTGGGAGAG CAGGCGTGGG CAAGTCAGCT CTTGTAGTGA 180
 GATTTCTGAC CAAACGGTTC ATCTGGGAAT ATGATCCAC CCTCGAATCA ACCTACCGAC 240
 ACCAAGCAAC CATCGATGAT GAAGTTGTTT CCATGGAGAT ACTAGACACT GCTGGTCAGG 300
 AAGATACCAT TCAGAGGGAG GGGCACATGC GATGGGGGGA AGGCTTTGTG CTGGTCTACG 360
 ACATTACTGA CCGAGGAAGT TTTGAGGAAG TGCTGCCACT TAAGAACATC CTAGATGAGA 420
 TCAAAAAGCC CAAGAATGTG ACTCTCATCT TGTTGGAAA CAAAGCTGAC TTGGACCACT 480
 CCAGGCAGGT TAGCACAGAA GAAGGAGAGA AGCTGGCCAC AGAATTGGCT TGTGCTTTTT 540
 ACGAGTGCTC TGCCTGCACT GGAGAAGGGA ATATCACAGA GATATTCTAT GAATTGTGTC 600
 GAGAGGTGCG TCGCCGGAGG ATGGTGCAGG GCAAGACGAG GCGACGCAGC TCCACCACGC 660
 ATGTCAAGCA AACCATTAAC GAGATGCTCA CCAAAATCAG TAGTTAGGCA GCCCAGCTGA 720
 GGTGACCAA CTAATTGGAA CACTCTTCCC CTTCTGTTCC CCTTCNGAAT AAAACCAAAT 780
 ATGCATTCCN TGTTTGGATT CTGAGAAATT CTGGGCTTCC ATTGT 825

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 190877

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Ala Ala Ala Gly Gly Arg Leu Arg Gln Glu Lys Tyr Arg Leu
 1           5           10           15
Val Val Val Gly Gly Gly Val Gly Lys Ser Ala Leu Thr Ile Gln
      20           25           30
Phe Ile Gln Ser Tyr Phe Val Thr Asp Tyr Asp Pro Thr Ile Glu Asp
      35           40           45
Ser Tyr Thr Lys Gln Cys Val Ile Asp Asp Arg Ala Ala Arg Leu Asp
      50           55           60
Ile Leu Asp Thr Ala Gly Gln Glu Glu Phe Gly Ala Met Arg Glu Gln
      65           70           75           80
Tyr Met Arg Thr Gly Glu Gly Phe Leu Leu Val Phe Ser Val Thr Asp
      85           90           95
Arg Gly Ser Phe Glu Glu Ile Tyr Lys Phe Gln Arg Gln Ile Leu Arg
      100          105          110
Val Lys Asp Arg Asp Glu Phe Pro Met Ile Leu Ile Gly Asn Lys Ala
      115          120          125
Asp Leu Asp His Gln Arg Gln Val Thr Gln Glu Glu Gly Gln Gln Leu
      130          135          140
Ala Arg Gln Leu Lys Val Thr Tyr Met Glu Ala Ser Ala Lys Ile Arg
      145          150          155          160
Met Asn Val Asp Gln Ala Phe His Glu Leu Val Arg Val Ile Arg Lys
      165          170          175
Phe Gln Glu Gln Glu Cys Pro Pro Ser Pro Glu Pro Thr Arg Lys Glu
      180          185          190
Lys Asp Lys Lys Gly Cys His Cys Val Ile Phe
      195          200

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 1656005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Glu Ser Gly Ala Arg Pro Ile Gly Ser Ser Cys Ser Ser Pro Ala
 1           5           10           15
Ala Leu Ser Arg Glu Tyr Lys Leu Val Met Leu Gly Ala Gly Gly Val
      20           25           30
Gly Lys Ser Ala Met Thr Met Gln Phe Ile Ser His Arg Phe Pro Glu
      35           40           45
Asp His Asp Pro Thr Ile Glu Asp Ala Tyr Lys Ile Arg Ile Arg Ile
      50           55           60

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Asp	Asp	Glu	Pro	Ala	Asn	Leu	Asp	Ile	Leu	Asp	Thr	Ala	Gly	Gln	Ala	65	70	75	80
Glu	Phe	Thr	Ala	Met	Arg	Asp	Gln	Tyr	Met	Arg	Ala	Gly	Glu	Gly	Phe	85	90	95	
Ile	Ile	Cys	Tyr	Ser	Ile	Thr	Asp	Arg	Arg	Ser	Phe	His	Glu	Val	Arg	100	105	110	
Glu	Phe	Lys	Gln	Leu	Ile	Tyr	Arg	Val	Arg	Arg	Thr	Asp	Asp	Thr	Pro	115	120	125	
Val	Val	Leu	Val	Gly	Asn	Lys	Ser	Asp	Leu	Lys	Gln	Leu	Arg	Gln	Val	130	135	140	
Ser	Lys	Glu	Glu	Gly	Leu	Ser	Leu	Ala	Arg	Glu	Phe	Ser	Cys	Pro	Phe	145	150	155	160
Phe	Glu	Thr	Ser	Ala	Ala	Tyr	Arg	Tyr	Tyr	Ile	Asp	Asp	Val	Phe	His	165	170	175	
Ala	Leu	Val	Arg	Glu	Ile	Arg	Lys	Lys	Glu	Lys	Glu	Leu	Val	Leu	Ala	180	185	190	
Met	Glu	Lys	Lys	Ala	Lys	Pro	Lys	Asn	Ser	Val	Trp	Lys	Arg	Leu	Lys	195	200	205	
Ser	Pro	Phe	Arg	Arg	Lys	Lys	Asp	Ser	Val	Thr						210	215		